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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 15

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8598 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Rattus rattus

(G) CELL TYPE: pheochromocytoma

(H) CELL LINE: PC12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GGCACGAGCG GCACGAGGCG GTAGCTGAGG CGGTGGCCGA AGCCGCGCGA ACCTCAGGGC   60
AAGATGCTTG GGACAGGCCC TGCCACGGCC ACCGCCGGTG CCGCCACATC TAGCAACGTG   120
AGCGTTCTGC AGCAGTTCGC CAGTGGGCTG AAGAGCCGGA ATGAGGAGAC CAGGGCCAAA   180
GCAGCCAAGG AGCTCCAGCA CTATGTCACC ATGGAAC TTC GAGAGATGAG TCAGGAGGAG   240
TCTACTCGCT TCTATGACCA GCTGAACCAT CACATTTTTC AACTGGTTTC CAGCTCAGAC   300
GCCAATGAGA GGAAGGGTGG CATCTTGCC ATTGCCAGCC TCATTGGAGT GGAAGGTGGG   360
AATTCACCA GGATTGGCAG ATTTGCCAAC TACCTTCGGA ACCTCCTCCC CTCAGTGAT   420
CCAGTTGTCA TGGAGATGGC ATCCAAGGCC ATTGGCCGCC TTGCAATGGC AGGGGACACT   480
TTCAC TGCTG AGTATGTGGA GTTTGAAGTG AAGCGAGCCT TGGAGTGGCT GGGTGCTGAC   540
CGAAATGAGG GCCCGAGACA TGCAGCTGTC CTCGTTCTCC GTGAGCTGGC CATCAGCGTC   600
CCCACCTTCT TCTTCCAGCA AGTTCAGCCC TTCTTTGACA ACATTTTGTG GGCTGTGTGG   660
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GAGCGTCTGA GAGAGGAGAT GGAGGAAATC ACCCAGCAGC AGCTGGTACA TGACAAGTAC   960
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CAGGCTGTGC AGCCCCAGCA GTCAAACGCC TTGGTGGGAC TGCTGGGGTA CAGCTCCAC  1080
CAAGGCCTAA TGGGGTTTGG GGCTTCCCC AGCCCTACAA AGTCCACTCT GGTGGAAGC  1140
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TGTAGGAGCA GCAAGAACTC ACTGATCCAA ATGACAATCC TTAATCTGTT GCCCGGCTTG  1260
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GTCCTGAGCT GTGTCAAGAA GGAAGAGGAA CGGACCGCAG CGTTCCAGGC CCTAGGGCTG  1380
CTTCTGTGG CGGTGAGGTC CGAGTTTAAG GTCTACCTGC CCCGAGTACT TGACATCATC  1440
CGAGCAGCCC TGCCTCCAAA GGAAGTTGCC CACAAGAGGC AGAAACTGT GCAGGTGGAT  1500

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GACATCAAGG AGCTGCTGGA GCCCATGTTG GCASTGGGCC TGAGCCCTGC GCTCACTGCT	1620
GTGCTCTATG ACCTGAGCCG GCAGATTCCG CAGCTGAAGA AAGATATTCA GGACGGGCTT	1680
CTGAAGATGC TGTCCCTGGT CCTTATGCAC AAACCCCTGC GGCACCCGGG CATGCCCAAA	1740
GGCCTGGCCC ACCAGCTGGC CTCCCCAGGT CTTACCACCC TCCCTGAGGC CAGCGACGTG	1800
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GATGAGCGCT TCGATGCCCC CTGGGCCAG GCAGAAAAC TACAAGCTCT GTTGTGGCT	2160
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GAGCTGGAGC ACASTGGCAT TGGGAGAATC AAGGAGCAGA GTGCCCCAT GCTGGGGCAC	2340
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CTCTTTGTCA TCATCATGGA CATGCTGCAG GACTCCTCTC TTCTGGCCAA AAGACAGGTG	2580
GCTTTGTGGA CCCTGGGACA GTTGGTGGCC AGTACTGGCT ACGTGGTGA GCCCTACAGG	2640
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ATCCAGCTGT TTGGCGCCAA CCTGGATGAC TATCTGCACT TGTGTTGCC TCCGATCGTG	3420
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CCTCAGCTCA TTGCAAGAAT TGACACGCCC AGACCCTTGG TGGGCCGGCT CATTCACCAG	5940
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GTGCCAGGAA	CATATGACCC	CAACCAGACA	ATCATTCGCA	TTCAGTCCAT	AGCCCCGTCT	6540
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CACGAGTTTG	TTTTCTCCT	GAAAGGCCAT	GAAGATCTGC	GGCAGGACGA	GCGAGTGATG	6660
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CTCAGCATCC	AGAGATACGC	CGTCATTCT	CTGTCCACCA	ACTCGGGCCT	GATTGGCTGG	6780
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CACCCATCCA	ACCTGATGCT	GGACCGGCTG	AGTGGAAAGA	TCCTGCACAT	TGACTTTGGG	7140
GACTGCTTTG	AGGTGCTAT	GACCAGAGAG	AAATTTCAG	AAAAGATTCC	ATTTAGACTA	7200
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GCCTTTGTCT	ATGACCTCT	GCTGAATTGG	AGGCTGATGG	ACACAAATGC	CAAAGGCAAC	7380
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GGTGTAGAAC	TTGGAGAACC	AGCCCATAA	AAAACAGGGA	CCACTGTGCC	AGAATCCATC	7500
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TTATGCCAAC	CTCCTAGCTG	CTGTTGAAAA	GACACTGTCA	GAAACACAAG	GCTTGATTCA	7920
GTTCCAGGA	CAGTGAAACA	CAGTAATCCT	ACAGAAACCA	AGCCTTTGAT	TTTGGGAGAA	7980
CAGAAGATGA	GTAAGTACT	AAGAAATACG	GGTTTGACT	TAACTTACAG	AAGAACTCAT	8040
CATACGCATT	TGCTGACCGA	ATAATCTAGT	TGATCCTCTC	AACGAGGGC	TTCAACAGCA	8100
AGGACACAGA	TGTCAGCACT	CCACCATCCT	GTTACCTCAC	CCGTCCCTGG	ATGCACTGGC	8160
AACATCTGCA	GGATGGGCCA	CGTGTGTGT	AAGAAGATCT	GTCTTCCACC	TGATCCCATG	8220
ATGCTGAACC	TCACAGAGCC	GGCCTTCCAG	GAGGACGTT	TGCTCAGACG	CCTGGCCACC	8280
GAGGATGAGC	AGGTGTGCCA	GGATCTCAGT	GCAGGGTCCA	CGCTGGCCCT	GCTGCTGTGT	8340
TCAGTGAGGG	ATGATATGT	TGTGTTTGCA	GCAGGGACTC	AGAACACAAA	TGCTTTGTG	8400
GAAGTGCTGA	TCTCAGAGGG	ACACTAGCGC	AGGTTGTGAA	TTAAGAGCAA	AGTAAATATC	8460
CAACTAAACA	CAAAGTATAA	GTGAAGCCAC	ATCTAGACAC	CATTGTATCT	GAGTAATTTT	8520
TGTGCCAATA	AATGACATCA	GAATTTTAAA	AGTAAAAAAA	ACGATATCAA	GCTTATCGAT	8580
ACCGTCGACC	TCGAGGGG					8598

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2549 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Rattus rattus
- (F) TISSUE TYPE: pheochromocytoma
- (G) CELL TYPE: PC12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Leu Gly Thr Gly Pro Ala Thr Ala Thr Ala Gly Ala Ala Thr Ser
1           5           10           15
Ser Asn Val Ser Val Leu Gln Gln Phe Ala Ser Gly Leu Lys Ser Arg
20           25           30
Asn Glu Glu Thr Arg Ala Lys Ala Ala Lys Glu Leu Gln His Tyr Val
35           40           45
Thr Met Glu Leu Arg Glu Met Ser Gln Glu Glu Ser Thr Arg Phe Tyr
50           55           60
Asp Gln Leu Asn His His Ile Phe Glu Leu Val Ser Ser Ser Asp Ala
65           70           75           80
Asn Glu Arg Lys Gly Gly Ile Leu Ala Ile Ala Ser Leu Ile Gly Val
85           90           95
Glu Gly Gly Asn Ser Thr Arg Ile Gly Arg Phe Ala Asn Tyr Leu Arg
100          105          110
Asn Leu Leu Pro Ser Ser Asp Pro Val Val Met Glu Met Ala Ser Lys
115          120          125
Ala Ile Gly Arg Leu Ala Met Ala Gly Asp Thr Phe Thr Ala Glu Tyr
130          135          140
Val Glu Phe Glu Val Lys Arg Ala Leu Glu Trp Leu Gly Ala Asp Arg
145          150          155          160
Asn Glu Gly Arg Arg His Ala Ala Val Leu Val Leu Arg Glu Leu Ala
165          170          175
Ile Ser Val Pro Thr Phe Phe Phe Gln Gln Val Gln Pro Phe Phe Asp
180          185          190
Asn Ile Phe Val Ala Val Trp Asp Pro Lys Gln Ala Ile Arg Glu Gly
195          200          205
Ala Val Ala Ala Leu Arg Ala Cys Leu Ile Leu Thr Thr Gln Arg Glu
210          215          220
Pro Lys Glu Met Gln Lys Pro Gln Trp Tyr Arg His Thr Phe Glu Glu
225          230          235          240
Ala Glu Lys Gly Phe Asp Glu Thr Leu Ala Lys Glu Lys Gly Met Asn
245          250          255
Arg Asp Asp Arg Ile His Gly Ala Leu Leu Ile Leu Asn Glu Leu Val
260          265          270
Arg Ile Ser Ser Met Glu Gly Glu Arg Leu Arg Glu Glu Met Glu Glu
275          280          285
Ile Thr Gln Gln Gln Leu Val His Asp Lys Tyr Cys Lys Asp Leu Met
290          295          300

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Gly	Phe	Gly	Thr	Lys	Pro	Arg	His	Ile	Thr	Pro	Phe	Thr	Ser	Phe	Gln
305					310					315					320
Ala	Val	Gln	Pro	Gln	Gln	Ser	Asn	Ala	Leu	Val	Gly	Leu	Leu	Gly	Tyr
		325							330					335	
Ser	Ser	His	Gln	Gly	Leu	Met	Gly	Phe	Gly	Ala	Ser	Pro	Ser	Pro	Thr
		340						345					350		
Lys	Ser	Thr	Leu	Val	Glu	Ser	Arg	Cys	Cys	Arg	Asp	Leu	Met	Glu	Glu
	355						360					365			
Lys	Phe	Asp	Gln	Val	Cys	Gln	Trp	Val	Leu	Lys	Cys	Arg	Ser	Ser	Lys
	370					375					380				
Asn	Ser	Leu	Ile	Gln	Met	Thr	Ile	Leu	Asn	Leu	Leu	Pro	Arg	Leu	Val
385					390					395					400
Ala	Phe	Arg	Pro	Ser	Ala	Phe	Thr	Asp	Thr	Gln	Tyr	Leu	Gln	Asp	Thr
			405						410					415	
Met	Asn	His	Val	Leu	Ser	Cys	Val	Lys	Lys	Glu	Lys	Glu	Arg	Thr	Ala
	420							425					430		
Ala	Phe	Gln	Ala	Leu	Gly	Leu	Leu	Ser	Val	Ala	Val	Arg	Ser	Glu	Phe
	435						440					445			
Lys	Val	Tyr	Leu	Pro	Arg	Val	Leu	Asp	Ile	Ile	Arg	Ala	Ala	Leu	Pro
	450					455					460				
Pro	Lys	Asp	Phe	Ala	His	Lys	Arg	Gln	Lys	Thr	Val	Gln	Val	Asp	Ala
465					470					475					480
Thr	Val	Phe	Thr	Cys	Ile	Ser	Met	Leu	Ala	Arg	Ala	Met	Gly	Pro	Gly
			485						490					495	
Ile	Gln	Gln	Asp	Ile	Lys	Glu	Leu	Leu	Glu	Pro	Met	Leu	Ala	Val	Gly
			500					505					510		
Leu	Ser	Pro	Ala	Leu	Thr	Ala	Val	Leu	Tyr	Asp	Leu	Ser	Arg	Gln	Ile
	515						520					525			
Pro	Gln	Leu	Lys	Lys	Asp	Ile	Gln	Asp	Gly	Leu	Leu	Lys	Met	Leu	Ser
	530					535					540				
Leu	Val	Leu	Met	His	Lys	Pro	Leu	Arg	His	Pro	Gly	Met	Pro	Lys	Gly
545				550						555					560
Leu	Ala	His	Gln	Leu	Ala	Ser	Pro	Gly	Leu	Thr	Thr	Leu	Pro	Glu	Ala
			565						570					575	
Ser	Asp	Val	Ala	Ser	Ile	Thr	Leu	Ala	Leu	Arg	Thr	Leu	Gly	Ser	Phe
		580						585					590		
Glu	Phe	Glu	Gly	His	Ser	Leu	Thr	Gln	Phe	Val	Arg	His	Cys	Ala	Asp
	595						600					605			
His	Phe	Leu	Asn	Ser	Glu	His	Lys	Glu	Ile	Arg	Met	Glu	Ala	Ala	Arg
	610					615					620				
Thr	Cys	Ser	Arg	Leu	Leu	Thr	Pro	Ser	Ile	His	Leu	Ile	Ser	Gly	His
625				630						635					640
Ala	His	Val	Val	Ser	Gln	Thr	Ala	Val	Gln	Val	Val	Ala	Asp	Val	Leu
			645						650					655	
Ser	Lys	Leu	Leu	Val	Val	Gly	Ile	Thr	Asp	Pro	Asp	Pro	Asp	Ile	Arg
		660						665					670		
Tyr	Cys	Val	Leu	Ala	Ser	Leu	Asp	Glu	Arg	Phe	Asp	Ala	His	Leu	Ala
		675					680					685			
Gln	Ala	Glu	Asn	Leu	Gln	Ala	Leu	Phe	Val	Ala	Leu	Asn	Asp	Gln	Val
	690					695						700			
Phe	Glu	Ile	Arg	Glu	Leu	Ala	Ile	Cys	Thr	Val	Gly	Arg	Leu	Ser	Ser
705				710						715					720
Met	Asn	Pro	Ala	Phe	Val	Met	Pro	Phe	Leu	Arg	Lys	Met	Leu	Ile	Gln

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725				730				735							
Ile	Leu	Thr	Glu	Leu	Glu	His	Ser	Gly	Ile	Gly	Arg	Ile	Lys	Glu	Gln
			740								745				750
Ser	Ala	Arg	Met	Leu	Gly	His	Leu	Val	Ser	Asn	Ala	Pro	Arg	Leu	Ile
			755								760				765
Arg	Pro	Tyr	Met	Glu	Pro	Ile	Leu	Lys	Ala	Leu	Ile	Leu	Lys	Leu	Lys
			770								775				780
Asp	Pro	Asp	Pro	Asp	Pro	Asn	Pro	Gly	Val	Ile	Asn	Asn	Val	Leu	Ala
			785								790				800
Thr	Ile	Gly	Glu	Leu	Ala	Gln	Val	Ser	Gly	Leu	Glu	Met	Arg	Lys	Trp
			805								810				815
Val	Asp	Glu	Leu	Phe	Val	Ile	Ile	Met	Asp	Met	Leu	Gln	Asp	Ser	Ser
			820								825				830
Leu	Leu	Ala	Lys	Arg	Gln	Val	Ala	Leu	Trp	Thr	Leu	Gly	Gln	Leu	Val
			835								840				845
Ala	Ser	Thr	Gly	Tyr	Val	Val	Glu	Pro	Tyr	Arg	Lys	Tyr	Pro	Thr	Leu
			850								855				860
Leu	Glu	Val	Leu	Leu	Asn	Phe	Leu	Lys	Thr	Glu	Gln	Asn	Gln	Gly	Thr
			865								870				875
Arg	Arg	Glu	Ala	Ile	Arg	Val	Leu	Gly	Leu	Leu	Gly	Ala	Leu	Asp	Pro
			885								890				895
Tyr	Lys	His	Lys	Val	Asn	Ile	Gly	Met	Ile	Asp	Gln	Ser	Arg	Asp	Ala
			900								905				910
Ser	Ala	Val	Ser	Leu	Ser	Glu	Ser	Lys	Ser	Ser	Gln	Asp	Ser	Ser	Asp
			915								920				925
Tyr	Ser	Thr	Ser	Glu	Met	Leu	Val	Asn	Met	Gly	Asn	Leu	Pro	Leu	Asp
			930								935				940
Glu	Phe	Tyr	Pro	Ala	Val	Ser	Met	Val	Ala	Leu	Met	Arg	Ile	Phe	Arg
			945								950				955
Asp	Gln	Ser	Leu	Ser	His	His	His	Thr	Met	Val	Val	Gln	Ala	Ile	Thr
			965								970				975
Phe	Ile	Phe	Lys	Ser	Leu	Gly	Leu	Lys	Cys	Val	Gln	Phe	Leu	Pro	Gln
			980								985				990
Val	Met	Pro	Thr	Phe	Leu	Asn	Val	Ile	Arg	Val	Cys	Asp	Gly	Ala	Ile
			995								1000				1005
Arg	Glu	Phe	Leu	Phe	Gln	Gln	Leu	Gly	Met	Leu	Val	Ser	Phe	Val	Lys
			1010								1015				1020
Ser	His	Ile	Arg	Pro	Tyr	Met	Asp	Glu	Ile	Val	Thr	Leu	Met	Arg	Glu
			1025								1030				1035
Phe	Trp	Val	Met	Asn	Thr	Ser	Ile	Gln	Ser	Thr	Ile	Ile	Leu	Leu	Ile
			1045								1050				1055
Glu	Gln	Ile	Val	Val	Ala	Leu	Gly	Gly	Glu	Phe	Lys	Leu	Tyr	Leu	Pro
			1060								1065				1070
Gln	Leu	Ile	Pro	His	Met	Leu	Arg	Val	Phe	Met	His	Asp	Asn	Ser	Gln
			1075								1080				1085
Gly	Arg	Ile	Val	Ser	Ile	Lys	Leu	Leu	Ala	Ala	Ile	Gln	Leu	Phe	Gly
			1090								1095				1100
Ala	Asn	Leu	Asp	Asp	Tyr	Leu	His	Leu	Leu	Leu	Pro	Pro	Ile	Val	Lys
			1105								1110				1115
Leu	Phe	Asp	Ala	Pro	Glu	Val	Pro	Leu	Pro	Ser	Arg	Lys	Ala	Ala	Leu
			1125								1130				1135
Glu	Thr	Val	Asp	Arg	Leu	Thr	Glu	Ser	Leu	Asp	Phe	Thr	Asp	Tyr	Ala
			1140								1145				1150

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Ser Arg Ile Ile His Pro Ile Val Arg Thr Leu Asp Gln Ser Pro Glu
 1155 1160 1165
 Leu Arg Ser Thr Ala Met Asp Thr Leu Ser Ser Leu Val Phe Gln Leu
 1170 1175 1180
 Gly Lys Lys Tyr Gln Ile Phe Ile Pro Met Val Asn Lys Val Leu Val
 1185 1190 1195 1200
 Arg His Arg Ile Asn His Gln Arg Tyr Asp Val Leu Ile Cys Arg Ile
 1205 1210 1215
 Val Lys Gly Tyr Thr Leu Ala Asp Glu Glu Glu Asp Pro Leu Ile Tyr
 1220 1225 1230
 Gln His Arg Met Leu Arg Ser Ser Gln Gly Asp Ala Leu Ala Ser Gly
 1235 1240 1245
 Pro Val Glu Thr Gly Pro Met Lys Lys Leu His Val Ser Thr Ile Asn
 1250 1255 1260
 Leu Gln Lys Ala Trp Gly Ala Ala Arg Arg Val Ser Lys Asp Asp Trp
 1265 1270 1275 1280
 Leu Glu Trp Leu Arg Arg Leu Ser Leu Glu Leu Leu Lys Asp Ser Ser
 1285 1290 1295
 Ser Pro Ser Leu Arg Ser Cys Trp Ala Leu Ala Gln Ala Tyr Asn Pro
 1300 1305 1310
 Met Ala Arg Asp Leu Phe Asn Ala Ala Phe Val Ser Cys Trp Ser Glu
 1315 1320 1325
 Leu Asn Glu Asp Gln Gln Asp Glu Leu Ile Arg Ser Ile Glu Leu Ala
 1330 1335 1340
 Leu Thr Ser Gln Asp Ile Ala Glu Val Thr Gln Thr Leu Leu Asn Leu
 1345 1350 1355 1360
 Ala Glu Phe Met Glu His Ser Asp Lys Gly Pro Leu Pro Leu Arg Asp
 1365 1370 1375
 Asp Asn Gly Ile Val Leu Leu Gly Glu Arg Ala Ala Lys Cys Arg Ala
 1380 1385 1390
 Tyr Ala Lys Ala Leu His Tyr Lys Glu Leu Glu Phe Gln Lys Gly Pro
 1395 1400 1405
 Thr Pro Ala Ile Leu Glu Ser Leu Ile Ser Ile Asn Asn Lys Leu Gln
 1410 1415 1420
 Gln Pro Glu Ala Ala Ser Gly Val Leu Glu Tyr Ala Met Lys His Phe
 1425 1430 1435 1440
 Gly Glu Leu Glu Ile Gln Ala Thr Trp Tyr Glu Lys Leu His Glu Trp
 1445 1450 1455
 Glu Asp Ala Leu Val Ala Tyr Asp Lys Lys Met Asp Thr Asn Lys Asp
 1460 1465 1470
 Asp Pro Glu Leu Met Leu Gly Arg Met Arg Cys Leu Glu Ala Leu Gly
 1475 1480 1485
 Glu Trp Gly Gln Leu His Gln Gln Cys Cys Glu Lys Trp Thr Leu Val
 1490 1495 1500
 Asn Asp Glu Thr Gln Ala Lys Met Ala Arg Met Ala Ala Ala Ala Ala
 1505 1510 1515 1520
 Trp Gly Leu Gly Gln Trp Asp Ser Met Glu Glu Tyr Thr Cys Met Ile
 1525 1530 1535
 Pro Arg Asp Thr His Asp Gly Ala Phe Tyr Arg Ala Val Leu Ala Leu
 1540 1545 1550
 His Gln Asp Leu Phe Ser Leu Ala Gln Gln Cys Ile Asp Lys Ala Arg
 1555 1560 1565

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Asp	Leu	Leu	Asp	Ala	Glu	Leu	Thr	Ala	Met	Ala	Gly	Glu	Ser	Tyr	Ser
1570						1575					1580				
Arg	Ala	Tyr	Gly	Ala	Met	Val	Ser	Cys	His	Met	Leu	Ser	Glu	Leu	Glu
1585						1590				1595					1600
Glu	Val	Ile	Gln	Tyr	Lys	Leu	Val	Pro	Glu	Arg	Arg	Glu	Ile	Ile	Arg
					1605					1610					1615
Gln	Ile	Trp	Trp	Glu	Arg	Leu	Gln	Gly	Cys	Gln	Arg	Ile	Val	Glu	Asp
					1620					1625					1630
Trp	Gln	Lys	Ile	Leu	Met	Val	Arg	Ser	Leu	Val	Val	Ser	Pro	His	Glu
					1635					1640					1645
Asp	Met	Arg	Thr	Trp	Leu	Lys	Tyr	Ala	Ser	Leu	Cys	Gly	Lys	Ser	Gly
					1650					1655					1660
Arg	Leu	Ala	Leu	Ala	His	Lys	Thr	Leu	Val	Leu	Leu	Gly	Val	Asp	
1665					1670					1675					1680
Pro	Ser	Arg	Gln	Leu	Asp	His	Pro	Leu	Pro	Thr	Val	His	Pro	Gln	Val
					1685					1690					1695
Thr	Tyr	Ala	Tyr	Met	Lys	Asn	Met	Trp	Lys	Ser	Ala	Arg	Lys	Ile	Asp
					1700					1705					1710
Ala	Phe	Gln	His	Met	Gln	His	Phe	Val	Gln	Thr	Met	Gln	Gln	Gln	Ala
					1715					1720					1725
Gln	His	Ala	Ile	Ala	Thr	Glu	Asp	Gln	Gln	His	Lys	Gln	Glu	Leu	His
					1730					1735					1740
Lys	Leu	Met	Ala	Arg	Cys	Phe	Leu	Lys	Leu	Gly	Glu	Trp	Gln	Leu	Asn
1745					1750					1755					1760
Leu	Gln	Gly	Ile	Asn	Glu	Ser	Thr	Ile	Pro	Lys	Val	Leu	Gln	Tyr	Tyr
					1765					1770					1775
Ser	Ala	Ala	Thr	Glu	His	Asp	Arg	Ser	Trp	Tyr	Lys	Ala	Trp	His	Ala
					1780					1785					1790
Trp	Ala	Val	Met	Asn	Phe	Glu	Ala	Val	Leu	His	Tyr	Lys	His	Gln	Asn
					1795					1800					1805
Gln	Ala	Arg	Asp	Glu	Lys	Lys	Lys	Leu	Arg	His	Ala	Ser	Gly	Ala	Asn
					1810					1815					1820
Ile	Thr	Asn	Ala	Thr	Thr	Thr	Ala	Thr	Thr	Ala	Ala	Ser	Ala	Ala	Ala
1825										1830					1835
Ala	Thr	Ser	Thr	Glu	Gly	Ser	Asn	Ser	Glu	Ser	Glu	Ala	Glu	Ser	Asn
					1845					1850					1855
Glu	Ser	Ser	Pro	Thr	Pro	Ser	Pro	Leu	Gln	Lys	Lys	Val	Thr	Glu	Asp
					1860					1865					1870
Leu	Ser	Lys	Thr	Leu	Leu	Leu	Tyr	Thr	Val	Pro	Ala	Val	Gln	Gly	Phe
					1875					1880					1885
Phe	Arg	Ser	Ile	Ser	Leu	Ser	Arg	Gly	Asn	Asn	Leu	Gln	Asp	Thr	Leu
					1890					1895					1900
Arg	Val	Leu	Thr	Leu	Trp	Phe	Asp	Tyr	Gly	His	Trp	Pro	Asp	Val	Asn
1905						1910				1915					1920
Glu	Ala	Leu	Val	Glu	Gly	Val	Lys	Ala	Ile	Gln	Ile	Asp	Thr	Trp	Leu
					1925					1930					1935
Gln	Val	Ile	Pro	Gln	Leu	Ile	Ala	Arg	Ile	Asp	Thr	Pro	Arg	Pro	Leu
					1940					1945					1950
Val	Gly	Arg	Leu	Ile	His	Gln	Leu	Leu	Thr	Asp	Ile	Gly	Arg	Tyr	His
					1955					1960					1965
Pro	Gln	Ala	Leu	Ile	Tyr	Pro	Leu	Thr	Val	Ala	Ser	Lys	Ser	Thr	Thr
					1970					1975					1980
Thr	Ala	Arg	His	Asn	Ala	Ala	Asn	Lys	Ile	Leu	Lys	Asn	Met	Cys	Glu

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1985	1990	1995	2000
His Ser Asn Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu 2005 2010 2015			
Ile Arg Val Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu 2020 2025 2030			
Glu Ala Ser Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe 2035 2040 2045			
Glu Val Leu Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr 2050 2055 2060			
Leu Lys Glu Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu 2065 2070 2075 2080			
Ala Gln Glu Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp 2085 2090 2095			
Leu Thr Gln Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser 2100 2105 2110			
Lys Gln Leu Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro 2115 2120 2125			
Lys Leu Leu Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr 2130 2135 2140			
Asp Pro Asn Gln Thr Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu 2145 2150 2155 2160			
Gln Val Ile Thr Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly 2165 2170 2175			
Ser Asn Gly His Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu 2180 2185 2190			
Arg Gln Asp Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu 2195 2200 2205			
Leu Ala Asn Asp Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg 2210 2215 2220			
Tyr Ala Val Ile Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val 2225 2230 2235 2240			
Pro His Cys Asp Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys 2245 2250 2255			
Lys Lys Ile Leu Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala 2260 2265 2270			
Pro Asp Tyr Asp His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu 2275 2280 2285			
His Ala Val Asn Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp 2290 2295 2300			
Leu Lys Ser Pro Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr 2305 2310 2315 2320			
Thr Arg Ser Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu 2325 2330 2335			
Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys 2340 2345 2350			
Ile Leu His Ile Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg 2355 2360 2365			
Glu Lys Phe Pro Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr 2370 2375 2380			
Asn Ala Met Glu Val Thr Gly Leu Asp Arg Asn Tyr Arg Thr Thr Cys 2385 2390 2395 2400			
His Thr Val Met Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala 2405 2410 2415			

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Val Leu Glu Ala Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met
2420 2425 2430

Asp Thr Asn Ala Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser
2435 2440 2445

Tyr Ser Ala Gly Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly
2450 2455 2460

Glu Pro Ala His Lys Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His
2465 2470 2475 2480

Ser Phe Ile Gly Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys
2485 2490 2495

Ala Ile Gln Ile Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp
2500 2505 2510

Phe Ser His Asp Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu
2515 2520 2525

Ile Lys Gln Ala Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly
2530 2535 2540

Trp Cys Pro Phe Trp
2545

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2470 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Pro His Glu Glu Gln Ile Trp Lys Ser Lys Leu Leu Lys Ala
1 5 10 15

Ala Asn Asn Asp Met Asp Met Asp Arg Asn Val Pro Leu Ala Pro Asn
20 25 30

Leu Asn Val Asn Met Asn Met Lys Met Asn Ala Ser Arg Asn Gly Asp
35 40 45

Glu Phe Gly Leu Thr Ser Ser Arg Phe Gly Gly Val Val Ile Gly Ser
50 55 60

Asn Gly Asp Val Asn Phe Lys Pro Ile Leu Glu Lys Ile Phe Arg Glu
65 70 75 80

Leu Thr Ser Asp Tyr Lys Glu Glu Arg Lys Leu Ala Ser Ile Ser Leu
85 90 95

Phe Asp Leu Leu Val Ser Leu Glu His Glu Leu Ser Ile Glu Glu Phe
100 105 110

Gln Ala Ile Ser Asn Asp Ile Asn Asn Lys Ile Leu Glu Leu Val His
115 120 125

Thr Lys Lys Thr Asn Thr Arg Val Gly Ala Val Leu Ser Ile Asp Thr
130 135 140

Leu Ile Ser Phe Tyr Ala Tyr Thr Glu Arg Leu Pro Asn Glu Thr Ser
145 150 155 160

Arg Leu Ala Gly Tyr Leu Arg Gly Leu Ile Pro Ser Asn Asp Val Glu
165 170 175

Val Met Arg Leu Ala Ala Lys Thr Leu Gly Lys Leu Ala Val Pro Gly
180 185 190

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Gly Thr Tyr Thr Ser Asp Phe Val Glu Phe Glu Ile Lys Ser Cys Leu
 195 200 205

Glu Trp Leu Thr Ala Ser Thr Glu Lys Asn Ser Phe Ser Ser Ser Lys
 210 215 220

Pro Asp His Ala Lys His Ala Ala Leu Leu Ile Ile Thr Ala Leu Ala
 225 230 235 240

Glu Asn Cys Pro Tyr Leu Leu Tyr Gln Tyr Leu Asn Ser Ile Leu Asp
 245 250 255

Asn Ile Trp Arg Ala Leu Arg Asp Pro His Leu Val Ile Arg Ile Asp
 260 265 270

Ala Ser Ile Thr Leu Ala Lys Cys Leu Ser Thr Leu Arg Asn Arg Asp
 275 280 285

Pro Gln Leu Thr Ser Gln Trp Val Gln Arg Leu Ala Thr Ser Cys Glu
 290 295 300

Tyr Gly Phe Gln Val Asn Thr Leu Glu Cys Ile His Ala Ser Leu Leu
 305 310 315 320

Val Tyr Lys Glu Ile Leu Phe Leu Lys Asp Pro Phe Leu Asn Gln Val
 325 330 335

Phe Asp Gln Met Cys Leu Asn Cys Ile Ala Tyr Glu Asn His Lys Ala
 340 345 350

Lys Met Ile Arg Glu Lys Ile Tyr Gln Ile Val Pro Leu Leu Ala Ser
 355 360 365

Phe Asn Pro Gln Leu Phe Ala Gly Lys Tyr Leu His Gln Ile Met Asp
 370 375 380

Asn Tyr Leu Glu Ile Leu Thr Asn Ala Pro Ala Lys Lys Ile Pro His
 385 390 395 400

Leu Lys Asp Asp Lys Pro Gln Ile Leu Ile Ser Ile Gly Asp Ile Ala
 405 410 415

Tyr Glu Val Gly Pro Asp Ile Ala Pro Tyr Val Lys Gln Ile Leu Asp
 420 425 430

Tyr Ile Glu His Asp Leu Gln Thr Lys Phe Lys Phe Arg Lys Lys Phe
 435 440 445

Glu Asn Glu Ile Phe Tyr Cys Ile Gly Arg Leu Ala Val Pro Leu Gly
 450 455 460

Pro Val Leu Gly Lys Leu Leu Asn Arg Asn Ile Leu Asp Leu Met Phe
 465 470 475 480

Lys Cys Pro Leu Ser Asp Tyr Met Gln Glu Thr Phe Gln Ile Leu Thr
 485 490 495

Glu Arg Ile Pro Ser Leu Gly Pro Lys Ile Asn Asp Glu Leu Leu Asn
 500 505 510

Leu Val Cys Ser Thr Leu Ser Gly Thr Pro Phe Ile Gln Pro Gly Ser
 515 520 525

Pro Met Glu Ile Pro Ser Phe Ser Arg Glu Arg Ala Arg Glu Trp Arg
 530 535 540

Asn Lys Ser Ile Leu Gln Lys Thr Gly Glu Ser Asn Asp Asp Asn Asn
 545 550 555 560

Asp Ile Lys Ile Ile Ile Gln Ala Phe Arg Met Leu Lys Asn Ile Lys
 565 570 575

Ser Arg Phe Ser Leu Val Glu Phe Val Arg Ile Val Ala Leu Ser Tyr
 580 585 590

Ile Glu His Thr Asp Pro Arg Val Arg Lys Leu Ala Ala Leu Thr Ser
 595 600 605

Cys Glu Ile Tyr Val Lys Asp Asn Ile Cys Lys Gln Thr Ser Leu His

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610	615	620
Ser Leu Asn Thr Val	Ser Glu Val Leu	Ser Lys Leu Leu Ala Ile Thr
625	630	635 640
Ile Ala Asp Pro Leu Gln Asp	Ile Arg Leu Glu Val Leu Lys Asn Leu	
645	650	655
Asn Pro Cys Phe Asp Pro Gln Leu Ala Gln Pro Asp Asn Leu Arg Leu		
660	665	670
Leu Phe Thr Ala Leu His Asp Glu Ser Phe Asn Ile Gln Ser Val Ala		
675	680	685
Met Glu Leu Val Gly Arg Leu Ser Ser Val Asn Pro Ala Tyr Val Ile		
690	695	700
Pro Ser Ile Arg Lys Ile Leu Leu Glu Leu Leu Thr Lys Leu Lys Phe		
705	710	715 720
Ser Thr Ser Ser Arg Glu Lys Glu Glu Thr Ala Ser Leu Leu Cys Thr		
725	730	735
Leu Ile Arg Ser Ser Lys Asp Val Ala Lys Pro Tyr Ile Glu Pro Leu		
740	745	750
Leu Asn Val Leu Leu Pro Lys Phe Gln Asp Thr Ser Ser Thr Val Ala		
755	760	765
Ser Thr Ala Leu Arg Thr Ile Gly Glu Leu Ser Val Val Gly Gly Glu		
770	775	780
Asp Met Lys Ile Tyr Leu Lys Asp Leu Phe Pro Leu Ile Ile Lys Thr		
785	790	795 800
Phe Gln Asp Gln Ser Asn Ser Phe Lys Arg Glu Ala Ala Leu Lys Ala		
805	810	815
Leu Gly Gln Leu Ala Ala Ser Ser Gly Tyr Val Ile Asp Pro Leu Leu		
820	825	830
Asp Tyr Pro Glu Leu Leu Gly Ile Leu Val Asn Ile Leu Lys Thr Glu		
835	840	845
Asn Ser Gln Asn Ile Arg Arg Gln Thr Val Thr Leu Ile Gly Ile Leu		
850	855	860
Gly Ala Ile Asp Pro Tyr Arg Gln Lys Glu Arg Glu Val Thr Ser Thr		
865	870	875 880
Thr Asp Ile Ser Thr Glu Gln Asn Ala Pro Pro Ile Asp Ile Ala Leu		
885	890	895
Leu Met Gln Gly Met Ser Pro Ser Asn Asp Glu Tyr Tyr Thr Val		
900	905	910
Val Ile His Cys Leu Leu Lys Ile Leu Lys Asp Pro Ser Leu Ser Ser		
915	920	925
Tyr His Thr Ala Val Ile Gln Ala Ile Met His Ile Phe Gln Thr Leu		
930	935	940
Gly Leu Lys Cys Val Ser Phe Leu Asp Gln Ile Ile Pro Thr Ile Leu		
945	950	955 960
Asp Val Met Arg Thr Cys Ser Gln Ser Leu Leu Glu Phe Tyr Phe Gln		
965	970	975
Gln Leu Cys Ser Leu Ile Ile Ile Val Arg Gln His Ile Arg Pro His		
980	985	990
Val Asp Ser Ile Phe Gln Ala Ile Lys Asp Phe Ser Ser Val Ala Lys		
995	1000	1005
Leu Gln Ile Thr Leu Val Ser Val Ile Glu Ala Ile Ser Lys Ala Leu		
1010	1015	1020
Glu Gly Glu Phe Lys Arg Leu Val Pro Leu Thr Leu Thr Phe Leu		
1025	1030	1035 1040

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Val Ile Leu Glu Asn Asp Lys Ser Ser Asp Lys Val Leu Ser Arg Arg
1045 1050 1055

Val Leu Arg Leu Leu Glu Ser Phe Gly Pro Asn Leu Glu Gly Tyr Ser
1060 1065 1070

His Leu Ile Thr Pro Lys Ile Val Gln Met Ala Glu Phe Thr Ser Gly
1075 1080 1085

Asn Leu Gln Arg Ser Ala Ile Ile Thr Ile Gly Lys Leu Ala Lys Asp
1090 1095 1100

Val Asp Leu Phe Glu Met Ser Ser Arg Ile Val His Ser Leu Leu Arg
1105 1110 1115 1120

Val Leu Ser Ser Thr Thr Ser Asp Glu Leu Ser Lys Val Ile Met Asn
1125 1130 1135

Thr Leu Ser Leu Leu Leu Ile Gln Met Gly Thr Ser Phe Ala Ile Phe
1140 1145 1150

Ile Pro Val Ile Asn Glu Val Leu Met Lys Lys His Ile Gln His Thr
1155 1160 1165

Ile Tyr Asp Asp Leu Thr Asn Arg Ile Leu Asn Asn Asp Val Leu Pro
1170 1175 1180

Thr Lys Ile Leu Glu Ala Asn Thr Thr Asp Tyr Lys Pro Ala Glu Gln
1185 1190 1195 1200

Met Glu Ala Ala Asp Ala Gly Val Ala Lys Leu Pro Ile Asn Gln Ser
1205 1210 1215

Val Leu Lys Ser Ala Trp Asn Ser Ser Gln Gln Arg Thr Lys Glu Asp
1220 1225 1230

Trp Gln Glu Trp Ser Lys Arg Leu Ser Ile Gln Leu Leu Lys Glu Ser
1235 1240 1245

Pro Ser His Ala Leu Arg Ala Cys Ser Asn Leu Ala Ser Met Tyr Tyr
1250 1255 1260

Pro Leu Ala Lys Glu Leu Phe Asn Thr Ala Phe Ala Cys Val Trp Thr
1265 1270 1275 1280

Glu Leu Tyr Ser Gln Tyr Gln Glu Asp Leu Ile Gly Ser Leu Cys Ile
1285 1290 1295

Ala Leu Ser Ser Pro Leu Asn Pro Pro Glu Ile His Gln Thr Leu Leu
1300 1305 1310

Asn Leu Val Glu Phe Met Glu His Asp Asp Lys Ala Leu Pro Ile Pro
1315 1320 1325

Thr Gln Ser Leu Gly Glu Tyr Ala Glu Arg Cys His Ala Tyr Ala Lys
1330 1335 1340

Ala Leu His Tyr Lys Glu Ile Lys Phe Ile Lys Glu Pro Glu Asn Ser
1345 1350 1355 1360

Thr Ile Glu Ser Leu Ile Ser Ile Asn Asn Gln Leu Asn Gln Thr Asp
1365 1370 1375

Ala Ala Ile Gly Ile Leu Lys His Ala Gln Gln His His Ser Leu Gln
1380 1385 1390

Leu Lys Glu Thr Trp Phe Glu Lys Leu Glu Arg Trp Glu Asp Ala Leu
1395 1400 1405

His Ala Tyr Asn Glu Arg Glu Lys Ala Gly Asp Thr Ser Val Ser Val
1410 1415 1420

Thr Leu Gly Lys Met Arg Ser Leu His Ala Leu Gly Glu Trp Glu Gln
1425 1430 1435 1440

Leu Ser Gln Leu Ala Ala Arg Lys Trp Lys Val Ser Lys Leu Gln Thr
1445 1450 1455

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Lys Lys Leu Ile Ala Pro Leu Ala Ala Gly Ala Arg Trp Gly Leu Gly
 1460 1465 1470
 Glu Trp Asp Met Leu Glu Gln Tyr Ile Ser Val Met Lys Pro Lys Ser
 1475 1480 1485
 Pro Asp Lys Glu Phe Phe Asp Ala Ile Leu Tyr Leu His Lys Asn Asp
 1490 1495 1500
 Tyr Asp Asn Ala Ser Lys His Ile Leu Asn Ala Arg Asp Leu Leu Val
 1505 1510 1515 1520
 Thr Glu Ile Ser Ala Leu Ile Asn Glu Ser Tyr Asn Arg Ala Tyr Ser
 1525 1530 1535
 Val Ile Val Arg Thr Gln Ile Ile Thr Glu Phe Glu Glu Ile Ile Lys
 1540 1545 1550
 Tyr Lys Gln Leu Pro Pro Asn Ser Glu Lys Lys Leu His Tyr Gln Asn
 1555 1560 1565
 Leu Trp Thr Lys Arg Leu Leu Gly Cys Gln Lys Asn Val Asp Leu Trp
 1570 1575 1580
 Gln Arg Val Leu Arg Val Arg Ser Leu Val Ile Lys Pro Lys Gln Asp
 1585 1590 1595 1600
 Leu Gln Ile Trp Ile Lys Phe Ala Asn Leu Cys Arg Lys Ser Gly Arg
 1605 1610 1615
 Met Arg Leu Ala Asn Lys Ala Leu Asn Met Leu Leu Glu Gly Gly Asn
 1620 1625 1630
 Asp Pro Ser Leu Pro Asn Thr Val Lys Ala Pro Pro Pro Val Val Tyr
 1635 1640 1645
 Ala Gln Leu Lys Tyr Ile Trp Ala Thr Gly Ala Tyr Lys Glu Ala Leu
 1650 1655 1660
 Asn His Leu Ile Gly Phe Thr Ser Arg Leu Ala His Asp Leu Gly Leu
 1665 1670 1675 1680
 Asp Pro Asn Asn Met Ile Ala Gln Ser Val Lys Leu Ser Ser Ala Ser
 1685 1690 1695
 Thr Ala Pro Tyr Val Glu Glu Tyr Thr Lys Leu Leu Ala Arg Cys Phe
 1700 1705 1710
 Leu Lys Gln Gly Glu Trp Arg Ile Ala Thr Gln Pro Asn Trp Arg Asn
 1715 1720 1725
 Thr Asn Pro Asp Ala Ile Leu Gly Ser Tyr Leu Leu Ala Thr His Phe
 1730 1735 1740
 Asp Lys Asn Trp Tyr Lys Ala Trp His Asn Trp Ala Leu Ala Asn Phe
 1745 1750 1755 1760
 Glu Val Ile Ser Met Val Gln Glu Glu Thr Lys Leu Asn Gly Gly Lys
 1765 1770 1775
 Asn Asp Asp Asp Asp Asp Thr Ala Val Asn Asn Asp Asn Val Arg Ile
 1780 1785 1790
 Asp Gly Ser Ile Leu Gly Ser Gly Ser Leu Thr Ile Asn Gly Asn Arg
 1795 1800 1805
 Tyr Pro Leu Glu Leu Ile Gln Arg His Val Val Pro Ala Ile Lys Gly
 1810 1815 1820
 Phe Phe His Ser Ile Ser Leu Leu Glu Thr Ser Cys Leu Gln Asp Thr
 1825 1830 1835 1840
 Leu Arg Leu Leu Thr Leu Leu Phe Asn Phe Gly Gly Ile Lys Glu Val
 1845 1850 1855
 Ser Gln Ala Met Tyr Glu Gly Phe Asn Leu Met Lys Ile Glu Asn Trp
 1860 1865 1870
 Leu Glu Val Leu Pro Gln Leu Ile Ser Arg Ile His Gln Pro Asp Pro

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1875	1880	1885
Thr Val Ser Asn Ser Leu Leu Ser Leu Leu Ser Asp Leu Gly Lys Ala 1890 1895 1900		
His Pro Gln Ala Leu Val Tyr Pro Leu Thr Val Ala Ile Lys Ser Glu 1905 1910 1915 1920		
Ser Val Ser Arg Gln Lys Ala Ala Leu Ser Ile Ile Glu Lys Ile Arg 1925 1930 1935		
Ile His Ser Pro Val Leu Val Asn Gln Ala Glu Leu Val Ser His Glu 1940 1945 1950		
Leu Ile Arg Val Ala Val Leu Trp His Glu Leu Trp Tyr Glu Gly Leu 1955 1960 1965		
Glu Asp Ala Arg Arg Gln Phe Phe Val Glu His Asn Ile Glu Lys Met 1970 1975 1980		
Phe Ser Thr Leu Glu Pro Leu His Lys His Leu Gly Asn Glu Pro Gln 1985 1990 1995 2000		
Thr Leu Ser Glu Val Ser Phe Gln Lys Ser Phe Gly Arg Asp Leu Asn 2005 2010 2015		
Asp Ala Tyr Glu Trp Leu Asn Asn Tyr Lys Lys Ser Lys Asp Ile Asn 2020 2025 2030		
Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val Phe Arg Lys Ile 2035 2040 2045		
Thr Arg Gln Ile Pro Gln Leu Gln Thr Leu Asp Leu Gln His Val Ser 2050 2055 2060		
Pro Gln Leu Leu Ala Thr His Asp Leu Glu Leu Ala Val Pro Gly Thr 2065 2070 2075 2080		
Tyr Phe Pro Gly Lys Pro Thr Ile Arg Ile Ala Lys Phe Glu Pro Leu 2085 2090 2095		
Phe Ser Val Ile Ser Ser Lys Gln Arg Pro Arg Lys Phe Ser Ile Lys 2100 2105 2110		
Gly Ser Asp Gly Lys Asp Tyr Lys Tyr Val Leu Lys Gly His Glu Asp 2115 2120 2125		
Ile Arg Gln Asp Ser Leu Val Met Gln Leu Phe Gly Leu Val Asn Thr 2130 2135 2140		
Leu Leu Lys Asn Asp Ser Glu Cys Phe Lys Arg His Leu Asp Ile Gln 2145 2150 2155 2160		
Gln Tyr Pro Ala Ile Pro Leu Ser Pro Lys Ser Gly Leu Leu Gly Trp 2165 2170 2175		
Val Pro Asn Ser Asp Thr Phe His Val Leu Ile Arg Glu His Arg Asp 2180 2185 2190		
Ala Lys Lys Ile Pro Leu Asn Ile Glu Gln Trp Val Met Leu Gln Met 2195 2200 2205		
Ala Pro Asp Tyr Glu Asn Leu Thr Leu Leu Gln Lys Ile Glu Val Phe 2210 2215 2220		
Thr Tyr Ala Leu Asp Asn Thr Lys Gly Gln Asp Leu Tyr Lys Ile Leu 2225 2230 2235 2240		
Trp Leu Lys Ser Arg Ser Ser Glu Thr Trp Leu Glu Arg Arg Thr Thr 2245 2250 2255		
Tyr Thr Arg Ser Leu Ala Val Met Ser Met Thr Gly Tyr Ile Leu Gly 2260 2265 2270		
Leu Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp Arg Ile Thr Gly 2275 2280 2285		
Lys Val Ile His Ile Asp Phe Gly Asp Cys Phe Glu Ala Ala Ile Leu 2290 2295 2300		

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Arg Glu Lys Tyr Pro Glu Lys Val Pro Phe Arg Leu Thr Arg Met Leu
 2305 2310 2315 2320
 Thr Tyr Ala Met Glu Val Ser Gly Ile Glu Gly Ser Phe Arg Ile Thr
 2325 2330 2335
 Cys Glu Asn Val Met Arg Val Leu Arg Asp Asn Lys Glu Ser Leu Met
 2340 2345 2350
 Ala Ile Leu Glu Ala Phe Ala Leu Asp Pro Leu Ile His Trp Gly Phe
 2355 2360 2365
 Asp Leu Pro Pro Gln Lys Leu Thr Glu Gln Thr Gly Ile Pro Leu Pro
 2370 2375 2380
 Leu Ile Asn Pro Ser Glu Leu Leu Arg Lys Gly Ala Ile Thr Val Glu
 2385 2390 2395 2400
 Glu Ala Ala Asn Met Glu Ala Glu Gln Gln Asn Glu Thr Arg Asn Ala
 2405 2410 2415
 Arg Ala Met Leu Val Leu Arg Arg Ile Thr Asp Lys Leu Thr Gly Asn
 2420 2425 2430
 Asp Ile Lys Arg Phe Asn Glu Leu Asp Val Pro Glu Gln Val Asp Lys
 2435 2440 2445
 Leu Ile Gln Gln Ala Thr Ser Ile Glu Arg Leu Cys Gln His Tyr Ile
 2450 2455 2460
 Gly Trp Cys Pro Phe Trp
 2465 2470

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2474 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Lys Tyr Ile Asn Lys Tyr Thr Thr Pro Pro Asn Leu Leu Ser
 1 5 10 15
 Leu Arg Gln Arg Ala Glu Gly Lys His Arg Thr Arg Lys Lys Leu Thr
 20 25 30
 His Lys Ser His Ser His Asp Asp Glu Met Ser Thr Thr Ser Asn Thr
 35 40 45
 Asp Ser Asn His Asn Gly Pro Asn Asp Ser Gly Arg Val Ile Thr Gly
 50 55 60
 Ser Ala Gly His Ile Gly Lys Ile Ser Phe Val Asp Ser Glu Leu Asp
 65 70 75 80
 Thr Thr Phe Ser Thr Leu Asn Leu Ile Phe Asp Lys Leu Lys Ser Asp
 85 90 95
 Val Pro Gln Glu Arg Ala Ser Gly Ala Asn Glu Leu Ser Thr Thr Leu
 100 105 110
 Thr Ser Leu Ala Arg Glu Val Ser Ala Glu Gln Phe Gln Arg Phe Ser
 115 120 125
 Asn Ser Leu Asn Asn Lys Ile Phe Glu Leu Ile His Gly Phe Thr Ser
 130 135 140
 Ser Glu Lys Ile Gly Gly Ile Leu Ala Val Asp Thr Leu Ile Ser Phe
 145 150 155 160

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Tyr Leu Ser Thr Glu Glu Leu Pro Asn Gln Thr Ser Arg Leu Ala Asn
 165 170 175
 Tyr Leu Arg Val Leu Ile Pro Ser Ser Asp Ile Glu Val Met Arg Leu
 180 185 190
 Ala Ala Asn Thr Leu Gly Arg Leu Thr Val Pro Gly Gly Thr Leu Thr
 195 200 205
 Ser Asp Phe Val Glu Phe Glu Val Arg Thr Cys Ile Asp Trp Leu Thr
 210 215 220
 Leu Thr Ala Asp Asn Asn Ser Ser Ser Ser Lys Leu Glu Tyr Arg Arg
 225 230 235 240
 His Ala Ala Leu Leu Ile Ile Lys Ala Leu Ala Asp Asn Ser Pro Tyr
 245 250 255
 Leu Leu Tyr Pro Tyr Val Asn Ser Ile Leu Asp Asn Ile Trp Val Pro
 260 265 270
 Leu Arg Asp Ala Lys Leu Ile Ile Arg Leu Asp Ala Ala Val Ala Leu
 275 280 285
 Gly Lys Cys Leu Thr Ile Ile Gln Asp Arg Asp Pro Ala Leu Gly Lys
 290 295 300
 Gln Trp Phe Gln Arg Leu Phe Gln Gly Cys Thr His Gly Leu Ser Leu
 305 310 315 320
 Asn Thr Asn Asp Ser Val His Ala Thr Leu Leu Val Phe Arg Glu Leu
 325 330 335
 Leu Ser Leu Lys Ala Pro Tyr Leu Arg Asp Lys Tyr Asp Asp Ile Tyr
 340 345 350
 Lys Ser Thr Met Lys Tyr Lys Glu Tyr Lys Phe Asp Val Ile Arg Arg
 355 360 365
 Glu Val Tyr Ala Ile Leu Pro Leu Leu Ala Ala Phe Asp Pro Ala Ile
 370 375 380
 Phe Thr Lys Lys Tyr Leu Asp Arg Ile Met Val His Tyr Leu Arg Tyr
 385 390 395 400
 Leu Lys Asn Ile Asp Met Asn Ala Ala Asn Asn Ser Asp Lys Pro Phe
 405 410 415
 Ile Leu Val Ser Ile Gly Asp Ile Ala Phe Glu Val Gly Ser Ser Ile
 420 425 430
 Ser Pro Tyr Met Thr Leu Ile Leu Asp Asn Ile Arg Glu Gly Leu Arg
 435 440 445
 Thr Lys Phe Lys Val Arg Lys Gln Phe Glu Lys Asp Leu Phe Tyr Cys
 450 455 460
 Ile Gly Lys Leu Ala Cys Ala Leu Gly Pro Ala Phe Ala Lys His Leu
 465 470 475 480
 Asn Lys Asp Leu Leu Asn Leu Met Leu Asn Cys Pro Met Ser Asp His
 485 490 495
 Met Gln Glu Thr Leu Met Ile Leu Asn Glu Lys Ile Pro Ser Leu Glu
 500 505 510
 Ser Thr Val Asn Ser Arg Ile Leu Asn Leu Leu Ser Ile Ser Leu Ser
 515 520 525
 Gly Glu Lys Phe Ile Gln Ser Asn Gln Tyr Asp Phe Asn Asn Gln Phe
 530 535 540
 Ser Ile Glu Lys Ala Arg Lys Ser Arg Asn Gln Ser Phe Met Lys Lys
 545 550 555 560
 Thr Gly Glu Ser Asn Asp Asp Ile Thr Asp Ala Gln Ile Leu Ile Gln
 565 570 575
 Cys Phe Lys Met Leu Gln Leu Ile His His Gln Tyr Ser Leu Thr Glu

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580	585	590
Phe Val Arg Leu Ile Thr Ile Ser Tyr Ile Glu His Glu Asp Ser Ser 595 600 605		
Val Arg Lys Leu Ala Ala Leu Thr Ser Cys Asp Leu Phe Ile Lys Asp 610 615 620		
Asp Ile Cys Lys Gln Thr Ser Val His Ala Leu His Ser Val Ser Glu 625 630 635 640		
Val Leu Ser Lys Leu Leu Met Ile Ala Ile Thr Asp Pro Val Ala Glu 645 650 655		
Ile Arg Leu Glu Ile Leu Gln His Leu Gly Ser Asn Phe Asp Pro Gln 660 665 670		
Leu Ala Gln Pro Asp Asn Leu Arg Leu Leu Phe Met Ala Leu Asn Asp 675 680 685		
Glu Ile Phe Gly Ile Gln Leu Glu Ala Ile Lys Ile Ile Gly Arg Leu 690 695 700		
Ser Ser Val Asn Pro Ala Tyr Val Val Pro Ser Leu Arg Lys Thr Leu 705 710 715 720		
Leu Glu Leu Leu Thr Gln Leu Lys Phe Ser Asn Met Pro Lys Lys Lys 725 730 735		
Glu Glu Ser Ala Thr Leu Leu Cys Thr Leu Ile Asn Ser Ser Asp Glu 740 745 750		
Val Ala Lys Pro Tyr Ile Asp Pro Ile Leu Asp Val Ile Leu Pro Lys 755 760 765		
Cys Gln Asp Ala Ser Ser Ala Val Ala Ser Thr Ala Leu Lys Val Leu 770 775 780		
Gly Glu Leu Ser Val Val Gly Gly Lys Glu Met Thr Arg Tyr Leu Lys 785 790 795 800		
Glu Leu Met Pro Leu Ile Ile Asn Thr Phe Gln Asp Gln Ser Asn Ser 805 810 815		
Phe Lys Arg Asp Ala Ala Leu Thr Thr Leu Gly Gln Leu Ala Ala Ser 820 825 830		
Ser Gly Tyr Val Val Gly Pro Leu Leu Asp Tyr Pro Glu Leu Leu Gly 835 840 845		
Ile Leu Ile Asn Ile Leu Lys Thr Glu Asn Asn Pro His Ile Arg Arg 850 855 860		
Gly Thr Val Arg Leu Ile Gly Ile Leu Gly Ala Leu Asp Pro Tyr Lys 865 870 875 880		
His Arg Glu Ile Glu Val Thr Ser Asn Ser Lys Ser Ser Val Glu Gln 885 890 895		
Asn Ala Pro Ser Ile Asp Ile Ala Leu Leu Met Gln Gly Val Ser Pro 900 905 910		
Ser Asn Asp Glu Tyr Tyr Pro Thr Val Val Ile His Asn Leu Met Lys 915 920 925		
Ile Leu Asn Asp Pro Ser Leu Ser Ile His His Thr Ala Ala Ile Gln 930 935 940		
Ala Ile Met His Ile Phe Gln Asn Leu Gly Leu Arg Cys Val Ser Phe 945 950 955 960		
Leu Asp Gln Ile Ile Pro Gly Ile Ile Leu Val Met Arg Ser Cys Pro 965 970 975		
Pro Ser Gln Leu Asp Phe Tyr Phe Gln Gln Leu Gly Ser Leu Ile Ser 980 985 990		
Ile Val Lys Gln His Ile Arg Pro His Val Glu Lys Ile Tyr Gly Val 995 1000 1005		

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Ile Arg Glu Phe Phe Pro Ile Ile Lys Leu Gln Ile Thr Ile Ile Ser
 1010 1015 1020
 Val Ile Glu Ser Ile Ser Lys Ala Leu Glu Gly Glu Phe Lys Arg Phe
 1025 1030 1035 1040
 Val Pro Glu Thr Leu Thr Phe Phe Leu Asp Ile Leu Glu Asn Asp Gln
 1045 1050 1055
 Ser Asn Lys Arg Ile Val Pro Ile Arg Ile Leu Lys Ser Leu Val Thr
 1060 1065 1070
 Phe Gly Pro Asn Leu Glu Asp Tyr Ser His Leu Ile Met Pro Ile Val
 1075 1080 1085
 Val Arg Met Thr Glu Tyr Ser Ala Gly Ser Leu Lys Lys Ile Ser Ile
 1090 1095 1100
 Ile Thr Leu Gly Arg Leu Ala Lys Asn Ile Asn Leu Ser Glu Met Ser
 1105 1110 1115 1120
 Ser Arg Ile Val Gln Ala Leu Val Arg Ile Leu Asn Asn Gly Asp Arg
 1125 1130 1135
 Glu Leu Thr Lys Ala Thr Met Asn Thr Leu Ser Leu Leu Leu Gln
 1140 1145 1150
 Leu Gly Thr Asp Phe Val Val Phe Val Pro Val Ile Asn Lys Ala Leu
 1155 1160 1165
 Leu Arg Asn Arg Ile Gln His Ser Val Tyr Asp Gln Leu Val Asn Lys
 1170 1175 1180
 Leu Leu Asn Asn Glu Cys Leu Pro Thr Asn Ile Ile Phe Asp Lys Glu
 1185 1190 1195 1200
 Asn Glu Val Pro Glu Arg Lys Asn Tyr Glu Asp Glu Met Gln Val Thr
 1205 1210 1215
 Lys Leu Pro Val Asn Gln Asn Ile Leu Lys Asn Ala Trp Tyr Cys Ser
 1220 1225 1230
 Gln Gln Lys Thr Lys Glu Asp Trp Gln Glu Trp Ile Arg Arg Leu Ser
 1235 1240 1245
 Ile Gln Leu Leu Lys Glu Ser Pro Ser Ala Cys Leu Arg Ser Cys Ser
 1250 1255 1260
 Ser Leu Val Ser Val Tyr Tyr Pro Leu Ala Arg Glu Leu Phe Asn Ala
 1265 1270 1275 1280
 Ser Phe Ser Ser Cys Trp Val Glu Leu Gln Thr Ser Tyr Gln Glu Asp
 1285 1290 1295
 Leu Ile Gln Ala Leu Cys Lys Ala Leu Ser Ser Ser Glu Asn Pro Pro
 1300 1305 1310
 Glu Ile Tyr Gln Met Leu Leu Asn Leu Val Glu Phe Met Glu His Asp
 1315 1320 1325
 Asp Lys Pro Leu Pro Ile Pro Ile His Thr Leu Gly Lys Tyr Ala Gln
 1330 1335 1340
 Lys Cys His Ala Phe Ala Lys Ala Leu His Tyr Lys Glu Val Glu Phe
 1345 1350 1355 1360
 Leu Glu Glu Pro Lys Asn Ser Thr Ile Glu Ala Leu Ile Ser Ile Asn
 1365 1370 1375
 Asn Gln Leu His Gln Thr Asp Ser Ala Ile Gly Ile Leu Lys His Ala
 1380 1385 1390
 Gln Gln His Asn Glu Leu Gln Leu Lys Glu Thr Trp Tyr Glu Lys Leu
 1395 1400 1405
 Gln Arg Trp Glu Asp Ala Leu Ala Ala Tyr Asn Glu Lys Glu Ala Ala
 1410 1415 1420

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Gly	Glu	Asp	Ser	Val	Glu	Val	Met	Met	Gly	Lys	Leu	Arg	Ser	Leu	Tyr	1425	1430	1435	1440
Ala	Leu	Gly	Glu	Trp	Glu	Glu	Leu	Ser	Lys	Leu	Ala	Ser	Glu	Lys	Trp	1445	1450	1455	
Gly	Thr	Ala	Lys	Pro	Glu	Val	Lys	Lys	Ala	Met	Ala	Pro	Leu	Ala	Ala	1460	1465	1470	
Gly	Ala	Ala	Trp	Gly	Leu	Glu	Gln	Trp	Asp	Glu	Ile	Ala	Gln	Tyr	Thr	1475	1480	1485	
Ser	Val	Met	Lys	Ser	Gln	Ser	Pro	Asp	Lys	Glu	Phe	Tyr	Asp	Ala	Ile	1490	1495	1500	
Leu	Cys	Leu	His	Arg	Asn	Asn	Phe	Lys	Lys	Ala	Glu	Val	His	Ile	Phe	1505	1510	1515	1520
Asn	Ala	Arg	Asp	Leu	Leu	Val	Thr	Glu	Leu	Ser	Ala	Leu	Val	Asn	Glu	1525	1530	1535	
Ser	Tyr	Asn	Arg	Ala	Tyr	Asn	Val	Val	Val	Arg	Ala	Gln	Ile	Ile	Ala	1540	1545	1550	
Glu	Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Lys	Lys	Leu	Pro	Gln	Asn	Ser	Asp	1555	1560	1565	
Lys	Arg	Leu	Thr	Met	Arg	Glu	Thr	Trp	Asn	Thr	Arg	Leu	Leu	Gly	Cys	1570	1575	1580	
Gln	Lys	Asn	Ile	Asp	Val	Trp	Gln	Arg	Ile	Leu	Arg	Val	Arg	Ser	Leu	1585	1590	1595	1600
Val	Ile	Lys	Pro	Lys	Glu	Asp	Ala	Gln	Val	Arg	Ile	Lys	Phe	Ala	Asn	1605	1610	1615	
Leu	Cys	Arg	Lys	Ser	Gly	Arg	Met	Ala	Leu	Ala	Lys	Lys	Val	Leu	Asn	1620	1625	1630	
Thr	Leu	Leu	Glu	Glu	Thr	Asp	Asp	Pro	Asp	His	Pro	Asn	Thr	Ala	Lys	1635	1640	1645	
Ala	Ser	Pro	Pro	Val	Val	Tyr	Ala	Gln	Leu	Lys	Tyr	Leu	Trp	Ala	Thr	1650	1655	1660	
Gly	Leu	Gln	Asp	Glu	Ala	Leu	Lys	Gln	Leu	Ile	Asn	Phe	Thr	Ser	Arg	1665	1670	1675	1680
Met	Ala	His	Asp	Leu	Gly	Leu	Asp	Pro	Asn	Asn	Met	Ile	Ala	Gln	Ser	1685	1690	1695	
Val	Pro	Gln	Gln	Ser	Lys	Arg	Val	Pro	Arg	His	Val	Glu	Asp	Tyr	Thr	1700	1705	1710	
Lys	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Lys	Gln	Gly	Glu	Trp	Arg	Val	Cys	1715	1720	1725	
Leu	Gln	Pro	Lys	Trp	Arg	Leu	Ser	Asn	Pro	Asp	Ser	Ile	Leu	Gly	Ser	1730	1735	1740	
Tyr	Leu	Leu	Ala	Thr	His	Phe	Asp	Asn	Thr	Trp	Tyr	Lys	Ala	Trp	His	1745	1750	1755	1760
Asn	Trp	Ala	Leu	Ala	Asn	Phe	Glu	Val	Ile	Ser	Met	Leu	Thr	Ser	Val	1765	1770	1775	
Ser	Lys	Lys	Lys	Gln	Glu	Gly	Ser	Asp	Ala	Ser	Ser	Val	Thr	Asp	Ile	1780	1785	1790	
Asn	Glu	Phe	Asp	Asn	Gly	Met	Ile	Gly	Val	Asn	Thr	Phe	Asp	Ala	Lys	1795	1800	1805	
Glu	Val	His	Tyr	Ser	Ser	Asn	Leu	Ile	His	Arg	His	Val	Ile	Pro	Ala	1810	1815	1820	
Ile	Lys	Gly	Phe	Phe	His	Ser	Ile	Ser	Leu	Ser	Glu	Ser	Ser	Ser	Leu	1825	1830	1835	1840
Gln	Asp	Ala	Leu	Arg	Leu	Leu	Thr	Leu	Trp	Phe	Thr	Phe	Gly	Gly	Ile				

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1845	1850	1855
Pro Glu Ala Thr Gln Ala Met His Glu Gly Phe Asn Leu Ile Gln Ile 1860 1865 1870		
Gly Thr Trp Leu Glu Val Leu Pro Gln Leu Ile Ser Arg Ile His Gln 1875 1880 1885		
Pro Asn Gln Ile Val Ser Arg Ser Leu Leu Ser Leu Leu Ser Asp Leu 1890 1895 1900		
Gly Lys Ala His Pro Gln Ala Leu Val Tyr Pro Leu Met Val Ala Ile 1905 1910 1915 1920		
Lys Ser Glu Ser Leu Ser Arg Gln Lys Ala Ala Leu Ser Ile Ile Glu 1925 1930 1935		
Lys Met Arg Ile His Ser Pro Val Leu Val Asp Gln Ala Glu Leu Val 1940 1945 1950		
Ser His Glu Leu Ile Arg Met Ala Val Leu Trp His Glu Gln Trp Tyr 1955 1960 1965		
Glu Gly Leu Asp Asp Ala Ser Arg Gln Phe Phe Gly Glu His Asn Thr 1970 1975 1980		
Glu Lys Met Phe Ala Ala Leu Glu Pro Leu Tyr Glu Met Leu Lys Arg 1985 1990 1995 2000		
Gly Pro Glu Thr Leu Arg Glu Ile Ser Phe Gln Asn Ser Phe Gly Arg 2005 2010 2015		
Asp Leu Asn Asp Ala Tyr Glu Trp Leu Met Asn Tyr Lys Lys Ser Lys 2020 2025 2030		
Asp Val Ser Asn Leu Asn Gln Ala Trp Asp Ile Tyr Tyr Asn Val Phe 2035 2040 2045		
Arg Lys Ile Gly Lys Gln Leu Pro Gln Leu Gln Thr Leu Glu Leu Gln 2050 2055 2060		
His Val Ser Pro Lys Leu Leu Ser Ala His Asp Leu Glu Leu Ala Val 2065 2070 2075 2080		
Pro Gly Thr Arg Ala Ser Gly Gly Lys Pro Ile Val Lys Ile Ser Lys 2085 2090 2095		
Phe Glu Pro Val Phe Ser Val Ile Ser Ser Lys Gln Arg Pro Arg Lys 2100 2105 2110		
Phe Cys Ile Lys Gly Ser Asp Gly Lys Asp Tyr Lys Tyr Val Leu Lys 2115 2120 2125		
Gly His Glu Asp Ile Arg Gln Asp Ser Leu Val Met Gln Leu Phe Gly 2130 2135 2140		
Leu Val Asn Thr Leu Leu Gln Asn Asp Ala Glu Cys Phe Arg Arg His 2145 2150 2155 2160		
Leu Asp Ile Gln Gln Tyr Pro Ala Ile Pro Leu Ser Pro Lys Ser Gly 2165 2170 2175		
Leu Leu Gly Trp Val Pro Asn Ser Asp Thr Phe His Val Leu Ile Arg 2180 2185 2190		
Glu His Arg Glu Ala Lys Lys Ile Pro Leu Asn Ile Glu His Trp Val 2195 2200 2205		
Met Leu Gln Met Ala Pro Asp Tyr Asp Asn Leu Thr Leu Leu Gln Lys 2210 2215 2220		
Val Glu Val Phe Thr Tyr Ala Leu Asn Asn Thr Glu Gly Gln Asp Leu 2225 2230 2235 2240		
Tyr Lys Val Leu Trp Leu Lys Ser Arg Ser Ser Glu Thr Trp Leu Glu 2245 2250 2255		
Arg Arg Thr Thr Tyr Thr Arg Ser Leu Ala Val Met Ser Met Thr Gly 2260 2265 2270		

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Tyr Ile Leu Gly Leu Gly Asp Arg His Pro Ser Asn Leu Met Leu Asp
 2275 2280 2285
 Arg Ile Thr Gly Lys Val Ile His Ile Asp Phe Gly Asp Cys Phe Glu
 2290 2295 2300
 Ala Ala Ile Leu Arg Glu Lys Phe Pro Glu Lys Val Pro Phe Arg Leu
 2305 2310 2315 2320
 Thr Arg Met Leu Thr Tyr Ala Met Glu Val Ser Gly Ile Glu Gly Ser
 2325 2330 2335
 Phe Arg Ile Thr Cys Glu Asn Val Met Lys Val Leu Arg Asp Asn Lys
 2340 2345 2350
 Gly Ser Leu Met Ala Ile Leu Glu Ala Phe Ala Phe Asp Pro Leu Ile
 2355 2360 2365
 Asn Trp Gly Phe Asp Leu Pro Thr Lys Lys Ile Glu Glu Glu Thr Gly
 2370 2375 2380
 Ile Gln Leu Pro Val Met Asn Ala Asn Glu Leu Leu Ser Asn Gly Ala
 2385 2390 2395 2400
 Ile Thr Glu Glu Glu Val Gln Arg Val Glu Asn Glu His Lys Asn Ala
 2405 2410 2415
 Ile Arg Asn Ala Arg Ala Met Leu Val Leu Lys Arg Ile Thr Asp Lys
 2420 2425 2430
 Leu Thr Gly Asn Asp Ile Arg Arg Phe Asn Asp Leu Asp Val Pro Glu
 2435 2440 2445
 Gln Val Asp Lys Leu Ile Gln Gln Ala Thr Ser Val Glu Asn Leu Cys
 2450 2455 2460
 Gln His Tyr Ile Gly Trp Cys Pro Phe Trp
 2465 2470

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGATCCCG TCGAGTTCA GTTGAACATC GCGGTGCTTC TGTAGCCATG GGAGTGCAGG 60
 TGGA 64

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCGGAATT CTCATTCCAG TTTTAGAA 28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Tyr Asp Pro Asn Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Ile Asp Phe Gly Asp
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Asp Gln Val Phe Glu
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGCCACCAC GATTTGCT

18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCGGATCCCG TCGAGCTTCA GTTGAAC TAC GGC GTGCTTC TGTAGCCATG GCGCGGCCCG

60

TTCC

64

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCCGGAATT CTCAATCAAT ATCCACTA 28

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGGGATCCA CNTAYGAYCC NAAAYCARC 28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGAATTCR TCNCCRAART CDATRTG 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGGGATCCA AYGAYCARGT NTTYGA 26

What is claimed is:

1. An isolated, purified cDNA molecule which encodes RAFT1, a protein having the amino acid sequence as shown in SEQ ID NO:2 wherein the acronym RAFT connotes a rapamycin and FKBP12 target.
2. The isolated, purified cDNA molecule of claim 1 which comprises the nucleotide sequence as shown in SEQ ID NO:1, nucleotides 64-7710.
3. An isolated, purified intron-free DNA molecule consisting of at least 20 contiguous nucleotides encoding all or a portion of the amino acid sequence as shown in SEQ ID NO: 2.
4. An isolated, purified intron-free DNA molecule consisting of at least 20 contiguous nucleotides of the sequence as shown in SEQ ID NO: 1.
5. An isolated DNA molecule encoding a rat RAFT protein obtained by a method comprising the steps of:
 - (a) probing a library of rat cDNA sequences with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and
 - (b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein, wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.
6. An isolated DNA molecule encoding a rat RAFT protein obtained by a method comprising the steps of:
 - (a) amplifying a DNA sequence using (i) at least one primer which comprises at least 10 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1 and (ii) a template which comprises rat cDNA or mRNA; and
 - (b) isolating an amplified DNA sequence which contains a complete open reading frame encoding a polypeptide of about 2550 amino acids encoding a rat RAFT protein, wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

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7. An isolated DNA molecule encoding a rat RAFT protein identified by a process comprising the steps of:

- (a) annealing a set of mixed oligonucleotides to a rat cDNA library, each member of said set of mixed oligonucleotides encoding a sequence of at least six contiguous amino acids of the amino acid sequence shown in SEQ ID NO:2; and
- (b) isolating a rat cDNA molecule which (i) anneals to at least one member of the set of mixed oligonucleotides, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

8. An isolated DNA molecule encoding a rat RAFT protein according to claim 7, wherein two sets of mixed oligonucleotides are annealed.

9. An isolated DNA molecule having a nucleotide sequence, or a degenerate sequence thereof, obtained by a method comprising the steps of:

- (a) probing a library of rat cDNA molecules with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and
- (b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame

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encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

10. A method of isolating a DNA molecule encoding a mammalian RAFT protein comprising the steps of:

- (a) probing a library of rat cDNA sequences with a probe which comprises at least 15 contiguous nucleotides selected from the sequence shown in SEQ ID NO: 1; and
- (b) isolating a rat cDNA molecule which (i) hybridizes to the probe, (ii) contains a complete open reading frame encoding a polypeptide of about 2550 amino acids, and (iii) encodes a rat RAFT protein,

wherein said rat RAFT protein binds to FKBP12 in the presence of 1 to 10 nM rapamycin but not in the absence of 1 to 10 nM rapamycin.

11. The method of claim 10 wherein the probe comprises at least 20 contiguous nucleotides encoding all or a portion of the amino acid sequence as shown in SEQ ID NO:2.

12. The method of claim 10 wherein the probe comprises at least 20 contiguous nucleotides as shown in SEQ ID NO:1.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,492,106 B1
APPLICATION NO. : 08/305790
DATED : December 10, 2002
INVENTOR(S) : David M. Sabatini et al.

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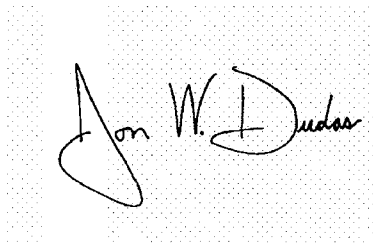
It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

On Title Page, should read, under (73) Assignee:

--Sloan-Kettering Institute for Cancer Research, New York, NY (US)-- has been inserted.

Signed and Sealed this

Seventeenth Day of October, 2006

A handwritten signature in black ink, reading "Jon W. Dudas", is centered within a rectangular area that has a light gray dotted background.

JON W. DUDAS
Director of the United States Patent and Trademark Office

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